

#6

SEQUENCE LISTING

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Boudolf, Veronique  
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Inze, Dirk

<120> NOVEL CELL CYCLE GENES AND USES THEREOF

<130> 2364/300

<140> 09/868,300

<141> 2001-06-15

<150> PCT/EP99/10084

<151> 1999-12-17

<150> EP 98 12 4062.5

<151> 1998-12-17

<160> 58

<170> PatentIn Ver. 2.1

<210> 1

<211> 1989

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<221> CDS

<222> (2)..(1669)

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Asp Asn Ala Ile Gln Arg Ala Leu Ile Val Gly Asp Tyr Lys Glu Ala

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gtg gat cag tgt ata act gca aat aag atg gcc gat gct tta gtt att 145

Val Asp Gln Cys Ile Thr Ala Asn Lys Met Ala Asp Ala Leu Val Ile

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Asn Asn Asp Leu Arg Ser Leu Ile Tyr Thr Arg Ser His Lys Phe Trp			
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aaa gag act ctt gct ctc ctc tgt act ttt gca caa gga gaa caa tgg			337
Lys Glu Thr Leu Ala Leu Leu Cys Thr Phe Ala Gln Gly Glu Gln Trp			
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aca acc ctg tgt gat gcc ctt gcc tcg aag ttg atg gct gct ggt aac			385
Thr Thr Leu Cys Asp Ala Leu Ala Ser Lys Leu Met Ala Ala Gly Asn			
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act ttg gct gca gtt ctc tgc tac att tgc gca ggc aat gtt gac aga			433
Thr Leu Ala Ala Val Leu Cys Tyr Ile Cys Ala Gly Asn Val Asp Arg			
	130	135	140
aca gta gaa att tgg tcg agg agc ctt gca aat gag cgg gat gga aga			481
Thr Val Glu Ile Trp Ser Arg Ser Leu Ala Asn Glu Arg Asp Gly Arg			
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tct tat gct gag ctt ctt caa gat ctt atg gag aag act ctt gtc ctt			529
Ser Tyr Ala Glu Leu Leu Gln Asp Leu Met Glu Lys Thr Leu Val Leu			
	165	170	175
gct ttg gca act ggc aac aaa aag ttc agc gca tct ctg tgt aaa ctc			577
Ala Leu Ala Thr Gly Asn Lys Lys Phe Ser Ala Ser Leu Cys Lys Leu			
	180	185	190
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Phe Glu Ser Tyr Ala Glu Ile Leu Ala Ser Gln Gly Leu Leu Thr Thr			
	195	200	205
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Ala Met Lys Tyr Leu Lys Val Leu Asp Ser Gly Gly Leu Ser Pro Glu			
	210	215	220
ctt tca ata tta cgt gat cgt att tct cta tct gca gaa cct gag act			721
Leu Ser Ile Leu Arg Asp Arg Ile Ser Leu Ser Ala Glu Pro Glu Thr			
	225	230	235
aac act aca gct tca gga aac act cag cct caa agc acc atg cca tat			769
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aat cag gag cca act cag gcg caa cca aac gtt ctt gct aac cca tat	817		
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Asp Asn Gln Tyr Gln Gln Pro Tyr Thr Asp Ser Tyr Tyr Val Pro Gln			
275	280	285	
gtt tca cat cca ccc atg cag caa cca acc atg ttt atg cca cac caa	913		
Val Ser His Pro Pro Met Gln Gln Pro Thr Met Phe Met Pro His Gln			
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gct cag cca gct ccg cag cca tct ttt act cca gct cct aca agc aat	961		
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gct cag cca tcc atg aga act aca ttt gtt cct tca act ccc cct gca	1009		
Ala Gln Pro Ser Met Arg Thr Thr Phe Val Pro Ser Thr Pro Pro Ala			
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Phe Thr Gly Pro Ser Asn Asn Ala Tyr Pro Val Pro Pro Gly Pro Gly			
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Gln Tyr Ala Pro Ser Gly Pro Ser Gln Leu Gly Gln Tyr Pro Asn Pro			
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ccc atg gca act cca gga gtt gct cca aga tct gtg caa cca gca agt	1249		
Pro Met Ala Thr Pro Gly Val Ala Pro Arg Ser Val Gln Pro Ala Ser			
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Pro Pro Thr Gln Gln Ala Ala Ala Gln Ala Ala Pro Ala Pro Ala Thr			
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Gln Lys Pro Val Ile Ala Thr Leu Thr Arg Leu Phe Asn Glu Thr Ser			
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Glu Ala Leu Gly Gly Ala Arg Ala Asn Thr Thr Lys Lys Arg Glu Ile			
465	470	475	480
gaa gac aac tcg aga aaa tta ggt gct ctg ttt gtg aaa ctc aac agc			1489
Glu Asp Asn Ser Arg Lys Leu Gly Ala Leu Phe Val Lys Leu Asn Ser			
	485	490	495
gga gac atc tcc aag aat gct gcg gac aaa ctc gca cag cta tgc caa			1537
Gly Asp Ile Ser Lys Asn Ala Ala Asp Lys Leu Ala Gln Leu Cys Gln			
	500	505	510
gct ctg gac aac aat gac ttc agc aca gcc ctt caa ata cag gta ctt			1585
Ala Leu Asp Asn Asn Asp Phe Ser Thr Ala Leu Gln Ile Gln Val Leu			
	515	520	525
ctg act acc agc gaa tgg gac gaa tgc aac ttc tgg ctg gca aca cta			1633
Leu Thr Thr Ser Glu Trp Asp Glu Cys Asn Phe Trp Leu Ala Thr Leu			
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Lys Arg Met Met Val Lys Ala Arg Gln Asn Val Arg			
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35 40 45

Ala His Val Gly Gly Thr Ala Leu Trp Glu Ser Thr Arg Glu Lys Tyr  
50 55 60

Leu Lys Thr Asn Ser Ala Pro Tyr Met Lys Val Val Ser Ala Met Val  
65 70 75 80

Asn Asn Asp Leu Arg Ser Leu Ile Tyr Thr Arg Ser His Lys Phe Trp  
85 90 95

Lys Glu Thr Leu Ala Leu Leu Cys Thr Phe Ala Gln Gly Glu Gln Trp  
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Thr Thr Leu Cys Asp Ala Leu Ala Ser Lys Leu Met Ala Ala Gly Asn  
115 120 125

Thr Leu Ala Ala Val Leu Cys Tyr Ile Cys Ala Gly Asn Val Asp Arg  
130 135 140

Thr Val Glu Ile Trp Ser Arg Ser Leu Ala Asn Glu Arg Asp Gly Arg  
145 150 155 160

Ser Tyr Ala Glu Leu Leu Gln Asp Leu Met Glu Lys Thr Leu Val Leu  
165 170 175

Ala Leu Ala Thr Gly Asn Lys Lys Phe Ser Ala Ser Leu Cys Lys Leu  
180 185 190

Phe Glu Ser Tyr Ala Glu Ile Leu Ala Ser Gln Gly Leu Leu Thr Thr  
195 200 205

Ala Met Lys Tyr Leu Lys Val Leu Asp Ser Gly Gly Leu Ser Pro Glu  
210 215 220

Leu Ser Ile Leu Arg Asp Arg Ile Ser Leu Ser Ala Glu Pro Glu Thr  
225 230 235 240

Asn Thr Thr Ala Ser Gly Asn Thr Gln Pro Gln Ser Thr Met Pro Tyr  
245 250 255

Asn Gln Glu Pro Thr Gln Ala Gln Pro Asn Val Leu Ala Asn Pro Tyr  
 260 265 270

Asp Asn Gln Tyr Gln Gln Pro Tyr Thr Asp Ser Tyr Tyr Val Pro Gln  
 275 280 285

Val Ser His Pro Pro Met Gln Gln Pro Thr Met Phe Met Pro His Gln  
 290 295 300

Ala Gln Pro Ala Pro Gln Pro Ser Phe Thr Pro Ala Pro Thr Ser Asn  
 305 310 315 320

Ala Gln Pro Ser Met Arg Thr Thr Phe Val Pro Ser Thr Pro Pro Ala  
 325 330 335

Leu Lys Asn Ala Asp Gln Tyr Gln Gln Pro Thr Met Ser Ser His Ser  
 340 345 350

Phe Thr Gly Pro Ser Asn Asn Ala Tyr Pro Val Pro Pro Gly Pro Gly  
 355 360 365

Gln Tyr Ala Pro Ser Gly Pro Ser Gln Leu Gly Gln Tyr Pro Asn Pro  
 370 375 380

Lys Met Pro Gln Val Val Ala Pro Ala Ala Gly Pro Ile Gly Phe Thr  
 385 390 395 400

Pro Met Ala Thr Pro Gly Val Ala Pro Arg Ser Val Gln Pro Ala Ser  
 405 410 415

Pro Pro Thr Gln Gln Ala Ala Ala Gln Ala Ala Pro Ala Pro Ala Thr  
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Pro Pro Pro Thr Val Gln Thr Ala Asp Thr Ser Asn Val Pro Ala His  
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Gln Lys Pro Val Ile Ala Thr Leu Thr Arg Leu Phe Asn Glu Thr Ser  
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Glu Ala Leu Gly Gly Ala Arg Ala Asn Thr Thr Lys Lys Arg Glu Ile  
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Glu Asp Asn Ser Arg Lys Leu Gly Ala Leu Phe Val Lys Leu Asn Ser  
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Gly Asp Ile Ser Lys Asn Ala Ala Asp Lys Leu Ala Gln Leu Cys Gln  
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Ala Leu Asp Asn Asn Asp Phe Ser Thr Ala Leu Gln Ile Gln Val Leu  
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Leu Arg Leu Gly Leu Ile Ile Glu Gly Lys Arg Leu Lys Lys Pro Pro  
20 25 30

act gtt ctc tca cgc ctc tct tct tct ctg gag aga tct ctg tta ctc 143  
Thr Val Leu Ser Arg Leu Ser Ser Ser Leu Glu Arg Ser Leu Leu Leu  
35 40 45

aat cat gat gac aag att ctg ctt gga tcg cca gac tct gtt acc gtg 191  
Asn His Asp Asp Lys Ile Leu Leu Gly Ser Pro Asp Ser Val Thr Val  
50 55 60

ttt gac ggg aga tct ccc cct gag atc agt att gca cac tac ttg gat 239  
Phe Asp Gly Arg Ser Pro Pro Glu Ile Ser Ile Ala His Tyr Leu Asp  
65 70 75

cgc att ttc aag tac tct tgc tgc agt ccc tcc tgc ttc gtc att gcg 287  
Arg Ile Phe Lys Tyr Ser Cys Cys Ser Pro Ser Cys Phe Val Ile Ala  
80 85 90 95

cat atc tac att gat cac ttt ctc cat aag acc cga gcc ctt ctc aaa 335  
His Ile Tyr Ile Asp His Phe Leu His Lys Thr Arg Ala Leu Leu Lys

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ccc ctt aat gtc cac cgc ctt atc att aca act gtc atg tta gct gct				383
Pro Leu Asn Val His Arg Leu Ile Ile Thr Thr Val Met Leu Ala Ala				
	115	120	125	
aaa gtc ttc gat gat agg tat ttc aac aat gca tac tac gca aga gtg				431
Lys Val Phe Asp Asp Arg Tyr Phe Asn Asn Ala Tyr Tyr Ala Arg Val				
	130	135	140	
gga ggt gtg act acg aga gag tta aac aga ttg gag atg gag ttg ttg				479
Gly Gly Val Thr Thr Arg Glu Leu Asn Arg Leu Glu Met Glu Leu Leu				
	145	150	155	
ttt acc ctt gac ttc aag ctt cag gta gat cct cag acg ttt cac aca				527
Phe Thr Leu Asp Phe Lys Leu Gln Val Asp Pro Gln Thr Phe His Thr				
160	165	170	175	
cac tgt tgt cag tta gaa aag cag aac aga gac ggc ttc cag atc gag				575
His Cys Cys Gln Leu Glu Lys Gln Asn Arg Asp Gly Phe Gln Ile Glu				
	180	185	190	
tgg ccc ata aaa gaa gca tgc cga gcc aac aaa gag act tgg cag aag				623
Trp Pro Ile Lys Glu Ala Cys Arg Ala Asn Lys Glu Thr Trp Gln Lys				
	195	200	205	
agg aca ccc gac tca ttc tgc tct caa acc aca gca cgc tga				665
Arg Thr Pro Asp Ser Phe Cys Ser Gln Thr Thr Ala Arg				
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tcggcaaggg taagatagga ttattttgtg ttttagtagt gatgattcctt ttgcatgatt				725
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Val Leu Ser Arg Leu Ser Ser Ser Leu Glu Arg Ser Leu Leu Leu Asn				



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His Asp Asp Lys Ile Leu Leu Gly Ser Pro Asp Ser Val Thr Val Phe		
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Asp Gly Arg Ser Pro Pro Glu Ile Ser Ile Ala His Tyr Leu Asp Arg		
65	70	75
Ile Phe Lys Tyr Ser Cys Cys Ser Pro Ser Cys Phe Val Ile Ala His		
85	90	95
Ile Tyr Ile Asp His Phe Leu His Lys Thr Arg Ala Leu Leu Lys Pro		
100	105	110
Leu Asn Val His Arg Leu Ile Ile Thr Thr Val Met Leu Ala Ala Lys		
115	120	125
Val Phe Asp Asp Arg Tyr Phe Asn Asn Ala Tyr Tyr Ala Arg Val Gly		
130	135	140
Gly Val Thr Thr Arg Glu Leu Asn Arg Leu Glu Met Glu Leu Leu Phe		
145	150	155
Thr Leu Asp Phe Lys Leu Gln Val Asp Pro Gln Thr Phe His Thr His		
165	170	175
Cys Cys Gln Leu Glu Lys Gln Asn Arg Asp Gly Phe Gln Ile Glu Trp		
180	185	190
Pro Ile Lys Glu Ala Cys Arg Ala Asn Lys Glu Thr Trp Gln Lys Arg		
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Leu Trp Gly Leu Ser His Gln Ile Phe Val Gly Cys Cys Ser Ser Val	
20 25 30	
atg gaa gat gat gct acc agc aaa tta gct gcc ccc aag ccc gag cct	144
Met Glu Asp Asp Ala Thr Ser Lys Leu Ala Ala Pro Lys Pro Glu Pro	
35 40 45	

gct gat cag aat ctc gaa gct ggc aaa gct gct gtc ttc caa agg gga	192
Ala Asp Gln Asn Leu Glu Ala Gly Lys Ala Ala Val Phe Gln Arg Gly	
50 55 60	
tac aat ttg gtt cag ggg aag tca gaa cat gga tta cca ttg gtt gat	240
Tyr Asn Leu Val Gln Gly Lys Ser Glu His Gly Leu Pro Leu Val Asp	
65 70 75 80	
aat tgc aaa gat ttg tcc tta gca gct ggt aac aat ttc gat gga acg	288
Asn Cys Lys Asp Leu Ser Leu Ala Ala Gly Asn Asn Phe Asp Gly Thr	
85 90 95	
gct cct ttg gag tat cat cag cag tat gat ctg caa caa gag ttt gaa	336
Ala Pro Leu Glu Tyr His Gln Gln Tyr Asp Leu Gln Gln Glu Phe Glu	
100 105 110	
cca aac ttc aat ggt ggt ttc aac aat tgt ccc agt tat ggt gta gta	384
Pro Asn Phe Asn Gly Gly Phe Asn Asn Cys Pro Ser Tyr Gly Val Val	
115 120 125	
gag ggt cct ata cat atc tct aat ttt atc ccg act att tgt cct cac	432
Glu Gly Pro Ile His Ile Ser Asn Phe Ile Pro Thr Ile Cys Pro His	
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cct ctg cat tct tgg gtc caa aaa tgt gct ctt tgg gat tgc cct agc	480
Pro Leu His Ser Trp Val Gln Lys Cys Ala Leu Trp Asp Cys Pro Ser	
145 150 155 160	
cag ctc agg gat ttg att ggg tcc agg att act gca gca gct tcc acg	528
Gln Leu Arg Asp Leu Ile Gly Ser Arg Ile Thr Ala Ala Ala Ser Thr	
165 170 175	
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Leu His Trp Leu Ser Asn Glu Arg Ala Thr Arg Tyr Glu Ser Gly Val	
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Ser Ala Lys Ala Gly Gly Lys Asp Val Gly Ile Pro Glu Cys Glu Gly	
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Ala Ala Thr Ala Lys Ser Pro Trp Asn Ala Pro Glu Leu Phe Asp Leu	
225 230 235 240	

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Thr Val Leu Glu Ser Glu Thr Leu Arg Glu Trp Leu Phe Phe Asp Lys	
245 250 255	
cca agg agg gcc ttt gag agc ggg aac aga aag caa aga tct tta cca	816
Pro Arg Arg Ala Phe Glu Ser Gly Asn Arg Lys Gln Arg Ser Leu Pro	
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gac tac aat ggt cgt ggt tgg cac gag tca cgt aaa cag atc atg gtc	864
Asp Tyr Asn Gly Arg Gly Trp His Glu Ser Arg Lys Gln Ile Met Val	
275 280 285	
gag ttt gga ggg ctg aag aga tct tac tac atg gat cca cag cct ctg	912
Glu Phe Gly Gly Leu Lys Arg Ser Tyr Tyr Met Asp Pro Gln Pro Leu	
290 295 300	
cac cat ttc gaa tgg cat ctt tac gaa tat gag atc aac aag tgt gat	960
His His Phe Glu Trp His Leu Tyr Glu Tyr Glu Ile Asn Lys Cys Asp	
305 310 315 320	
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Ala Cys Ala Leu Tyr Arg Leu Glu Leu Lys Leu Val Asp Gly Lys Lys	
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Thr Ser Lys Gly Lys Val Ser Asn Asp Ser Val Ala Asp Leu Gln Lys	
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cag atg gga aga ctc aca gct gag ttc cct cca gaa aac aat acc act	1104
Gln Met Gly Arg Leu Thr Ala Glu Phe Pro Pro Glu Asn Asn Thr Thr	
355 360 365	
aac acc acc aac aac aac aaa cgc tgc atc aaa gga aga cca aaa gtg	1152
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370 375 380	
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Ser Thr Lys Val Ala Thr Gly Asn Val Gln Asn Thr Val Glu Gln Ala	
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aat gac tat gga gta ggt gaa gag ttt aac tat ctg gtc gga aat cta	1248
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Met Glu Asp Asp Ala Thr Ser Lys Leu Ala Ala Pro Lys Pro Glu Pro  
35 40 45

Ala Asp Gln Asn Leu Glu Ala Gly Lys Ala Ala Val Phe Gln Arg Gly  
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Tyr Asn Leu Val Gln Gly Lys Ser Glu His Gly Leu Pro Leu Val Asp  
65 70 75 80

Asn Cys Lys Asp Leu Ser Leu Ala Ala Gly Asn Asn Phe Asp Gly Thr  
85 90 95

Ala Pro Leu Glu Tyr His Gln Gln Tyr Asp Leu Gln Gln Glu Phe Glu  
100 105 110

Pro Asn Phe Asn Gly Gly Phe Asn Asn Cys Pro Ser Tyr Gly Val Val  
115 120 125

Glu Gly Pro Ile His Ile Ser Asn Phe Ile Pro Thr Ile Cys Pro His  
130 135 140

Pro Leu His Ser Trp Val Gln Lys Cys Ala Leu Trp Asp Cys Pro Ser  
145 150 155 160

Gln Leu Arg Asp Leu Ile Gly Ser Arg Ile Thr Ala Ala Ala Ser Thr  
165 170 175

Leu His Trp Leu Ser Asn Glu Arg Ala Thr Arg Tyr Glu Ser Gly Val  
180 185 190

Arg Pro Gly Ser Ile Gly Leu Lys Asp Gly Leu Leu Phe Ala Ala Leu  
195 200 205

Ser Ala Lys Ala Gly Gly Lys Asp Val Gly Ile Pro Glu Cys Glu Gly  
210 215 220

Ala Ala Thr Ala Lys Ser Pro Trp Asn Ala Pro Glu Leu Phe Asp Leu  
 225 230 235 240  
 Thr Val Leu Glu Ser Glu Thr Leu Arg Glu Trp Leu Phe Phe Asp Lys  
 245 250 255  
 Pro Arg Arg Ala Phe Glu Ser Gly Asn Arg Lys Gln Arg Ser Leu Pro  
 260 265 270  
 Asp Tyr Asn Gly Arg Gly Trp His Glu Ser Arg Lys Gln Ile Met Val  
 275 280 285  
 Glu Phe Gly Gly Leu Lys Arg Ser Tyr Tyr Met Asp Pro Gln Pro Leu  
 290 295 300  
 His His Phe Glu Trp His Leu Tyr Glu Tyr Glu Ile Asn Lys Cys Asp  
 305 310 315 320  
 Ala Cys Ala Leu Tyr Arg Leu Glu Leu Lys Leu Val Asp Gly Lys Lys  
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 Thr Ser Lys Gly Lys Val Ser Asn Asp Ser Val Ala Asp Leu Gln Lys  
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 370 375 380  
 Ser Thr Lys Val Ala Thr Gly Asn Val Gln Asn Thr Val Glu Gln Ala  
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Met Asn Met Glu Val Asp Thr Val Thr Arg Lys Pro Arg Ile Leu Leu	
20 25 30	
gct gca agt gga agt gtg gct tca att aag ttc agt aat ctc tgc cat	144
Ala Ala Ser Gly Ser Val Ala Ser Ile Lys Phe Ser Asn Leu Cys His	
35 40 45	
tgt ttc tca gaa tgg gct gaa gtc aaa gcc gtc gct tca aaa tca tct	192
Cys Phe Ser Glu Trp Ala Glu Val Lys Ala Val Ala Ser Lys Ser Ser	
50 55 60	
ctc aat ttc gtt gat aaa cct tct cta cct cag aat gtg act ctc tat	240
Leu Asn Phe Val Asp Lys Pro Ser Leu Pro Gln Asn Val Thr Leu Tyr	
65 70 75 80	
aca gat gaa gat gaa tgg tct agc tgg aac aag att ggt gat ccc gtt	288
Thr Asp Glu Asp Glu Trp Ser Ser Trp Asn Lys Ile Gly Asp Pro Val	
85 90 95	
ctt cat atc gag ctc aga cgc tgg gct gat gtt atg atc att gct cct	336
Leu His Ile Glu Leu Arg Arg Trp Ala Asp Val Met Ile Ile Ala Pro	
100 105 110	
ttg tct gct aac aca tta gcc aag att gct ggt ggg tta tgt gat aat	384
Leu Ser Ala Asn Thr Leu Ala Lys Ile Ala Gly Gly Leu Cys Asp Asn	
115 120 125	
cta ttg aca tgt ata gta aga gca tgg gat tat agc aaa ccg ttg ttt	432
Leu Leu Thr Cys Ile Val Arg Ala Trp Asp Tyr Ser Lys Pro Leu Phe	
130 135 140	
gtt gca ccg gcg atg aac act ttg atg tgg aac aat cct ttc aca gaa	480
Val Ala Pro Ala Met Asn Thr Leu Met Trp Asn Asn Pro Phe Thr Glu	
145 150 155 160	
cgg cac ctt gtc ttg ctt gat gaa ctt gga atc acc cta att cct ccc	528
Arg His Leu Val Leu Leu Asp Glu Leu Gly Ile Thr Leu Ile Pro Pro	
165 170 175	

atc aag aag aaa ctg gcc tgt gga gac tac ggt aat ggc gca atg gct 576  
 Ile Lys Lys Lys Leu Ala Cys Gly Asp Tyr Gly Asn Gly Ala Met Ala  
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gag cct tct ctg att tat tcc act gtt aga ctg ttc tgg gag tca caa 624  
 Glu Pro Ser Leu Ile Tyr Ser Thr Val Arg Leu Phe Trp Glu Ser Gln  
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Ala Ala Ser Gly Ser Val Ala Ser Ile Lys Phe Ser Asn Leu Cys His  
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Cys Phe Ser Glu Trp Ala Glu Val Lys Ala Val Ala Ser Lys Ser Ser  
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Leu Asn Phe Val Asp Lys Pro Ser Leu Pro Gln Asn Val Thr Leu Tyr  
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Thr Asp Glu Asp Glu Trp Ser Ser Trp Asn Lys Ile Gly Asp Pro Val  
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Leu His Ile Glu Leu Arg Arg Trp Ala Asp Val Met Ile Ile Ala Pro  
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Leu Ser Ala Asn Thr Leu Ala Lys Ile Ala Gly Gly Leu Cys Asp Asn  
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Leu Leu Thr Cys Ile Val Arg Ala Trp Asp Tyr Ser Lys Pro Leu Phe  
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Val Ala Pro Ala Met Asn Thr Leu Met Trp Asn Asn Pro Phe Thr Glu  
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Arg His Leu Val Leu Leu Asp Glu Leu Gly Ile Thr Leu Ile Pro Pro  
165 170 175

Ile Lys Lys Lys Leu Ala Cys Gly Asp Tyr Gly Asn Gly Ala Met Ala  
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Leu Pro Tyr Arg His Ala Pro Arg Arg Pro Ile Ser Phe Ser Pro Val  
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Phe Ala Val His Ser Thr Asp Pro Lys Lys Ser Thr Gln Ser Ala Ser  
35 40 45

gct tcg gtt aaa tgg agt cta gag agt tgg aag tcg aag aaa gct ttg 251  
Ala Ser Val Lys Trp Ser Leu Glu Ser Trp Lys Ser Lys Lys Ala Leu  
50 55 60

caa ttg ccg gat tat cct acg ctt tct tct ttt cct cct ata gtt ttc 299  
Gln Leu Pro Asp Tyr Pro Thr Leu Ser Ser Phe Pro Pro Ile Val Phe  
65 70 75

gct ggt gag gct agg aaa cta gag gat aag ctt ggt caa gcg gct atg 347



Ala Gly Glu Ala Arg Lys Leu Glu Asp Lys Leu Gly Gln Ala Ala Met	
80 85 90 95	
ggt caa gcc ttt atg ctt caa ggt ggt gat tgt gct gag agt ttc aag	395
Gly Gln Ala Phe Met Leu Gln Gly Gly Asp Cys Ala Glu Ser Phe Lys	
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Glu Phe Asn Ala Asn Asn Ile Arg Asp Thr Phe Arg Val Leu Leu Gln	
115 120 125	
atg ggt gtt gtt ctc atg ttc ggt ggc cag tta cca gtt atc aag gtg	491
Met Gly Val Val Leu Met Phe Gly Gly Gln Leu Pro Val Ile Lys Val	
130 135 140	
gga aga atg gct ggt cag ttt gcg aag ccg aga tta gac cca ttt gag	539
Gly Arg Met Ala Gly Gln Phe Ala Lys Pro Arg Leu Asp Pro Phe Glu	
145 150 155	
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Glu Lys Asp Gly Val Lys Leu Pro Ser Tyr Arg Gly Asp Asn Ile Asn	
160 165 170 175	
ggt gat gct ttt gat gag aaa tcg agg att cct gat cct cat agg atg	635
Gly Asp Ala Phe Asp Glu Lys Ser Arg Ile Pro Asp Pro His Arg Met	
180 185 190	
gtt aga gcg tac aca cag tct gtg gct acg ttg aat ctc ttg aga gca	683
Val Arg Ala Tyr Thr Gln Ser Val Ala Thr Leu Asn Leu Leu Arg Ala	
195 200 205	
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Phe Ala Thr Gly Gly Tyr Ala Ala Met Gln Arg Val Ser Gln Trp Asn	
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Leu Asp Phe Thr Gln His Ser Glu Gln Gly Asp Arg Tyr Arg Glu Leu	
225 230 235	
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Ala Asn Arg Val Asp Glu Ala Leu Gly Phe Met Gly Ala Ala Gly Leu	
240 245 250 255	
act agt gct cac ccg atc atg act act act gag ttt tgg aca tcc cat	875
Thr Ser Ala His Pro Ile Met Thr Thr Thr Glu Phe Trp Thr Ser His	
260 265 270	
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Glu Cys Leu Leu Leu Pro Tyr Glu Gln Ala Leu Thr Arg Glu Asp Ser	
275	280 285
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Thr Ser Gly Leu Tyr Tyr Asp Cys Ser Ala His Met Leu Trp Val Gly	
290	295 300
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Glu Arg Thr Arg Gln Leu Asp Gly Ala His Val Glu Phe Leu Arg Gly	
305	310 315
atc gct aac ccc ctc gga atc aag gtg agt gat aaa atg gtc cct agt	1067
Ile Ala Asn Pro Leu Gly Ile Lys Val Ser Asp Lys Met Val Pro Ser	
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agg att acg gtt ata gtg aga atg gga gct gag aat atg cgg gtc aag	1163
Arg Ile Thr Val Ile Val Arg Met Gly Ala Glu Asn Met Arg Val Lys	
355	360 365
ctt cct aat ttg atc aga gca gtc cgt gga gcc ggt cag att gtg act	1211
Leu Pro Asn Leu Ile Arg Ala Val Arg Gly Ala Gly Gln Ile Val Thr	
370	375 380
tgg gtt agt gat cca atg cac gga aac aca atc atg gct cct ggt ggg	1259
Trp Val Ser Asp Pro Met His Gly Asn Thr Ile Met Ala Pro Gly Gly	
385	390 395
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Leu Lys Thr Arg Ser Phe Asp Ala Ile Arg Ala Glu Leu Arg Ala Phe	
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Phe Asp Val His Asp Gln Glu Gly Ser Phe Pro Gly Gly Val His Leu	
420	425 430
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Glu Met Thr Gly Gln Asn Val Thr Glu Cys Val Gly Gly Ser Arg Thr	
435	440 445
atc act tac aac gat cta agc tca cgc tac cac act cac tgt gac cca	1451
Ile Thr Tyr Asn Asp Leu Ser Ser Arg Tyr His Thr His Cys Asp Pro	
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aga ctc aac gca tct cag tct ctg gag ctt gca ttc atc att gca gag	1499

Arg Leu Asn Ala Ser Gln Ser Leu Glu Leu Ala Phe Ile Ile Ala Glu  
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 Arg Leu Arg Lys Arg Arg Leu Gly Ser Gly Asn Leu Pro Ser Ser Ile  
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 Gly Val  
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 Gly Glu Ala Arg Lys Leu Glu Asp Lys Leu Gly Gln Ala Ala Met Gly  
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 100 105 110  
 Phe Asn Ala Asn Asn Ile Arg Asp Thr Phe Arg Val Leu Leu Gln Met  
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Asn Phe Leu Asn Pro Pro Pro Pro Pro Arg Asn Gln Gly Leu Val Asp	
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gat gat gct gct tct gct gtt gtt tcc gac gag aat cgc aaa cca aca	144
Asp Asp Ala Ala Ser Ala Val Val Ser Asp Glu Asn Arg Lys Pro Thr	
35 40 45	
act gag att aaa gat ttc cag atc gtg gtc tct gct tcc gac aaa gaa	192
Thr Glu Ile Lys Asp Phe Gln Ile Val Val Ser Ala Ser Asp Lys Glu	
50 55 60	
cca aac aag aag agt cag aat cag aac cag ctt ggt cct aag aga agc	240
Pro Asn Lys Lys Ser Gln Asn Gln Asn Gln Leu Gly Pro Lys Arg Ser	
65 70 75 80	
tct aac aaa gac aga cac act aaa gtc gaa ggt aga ggt cga cga att	288
Ser Asn Lys Asp Arg His Thr Lys Val Glu Gly Arg Gly Arg Arg Ile	
85 90 95	
cgg atg cct gct ctt tgt gct gct agg att ttt caa ttg act aga gaa	336
Arg Met Pro Ala Leu Cys Ala Ala Arg Ile Phe Gln Leu Thr Arg Glu	
100 105 110	
ttg ggt cat aaa tct gat ggt gaa act atc cag tgg ctg ctt caa caa	384
Leu Gly His Lys Ser Asp Gly Glu Thr Ile Gln Trp Leu Leu Gln Gln	
115 120 125	
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Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Ser Gly Thr Ile Pro Ala	
130 135 140	
tct gct tta gct tct tca gct gca acc tct aac cat cat caa ggt ggg	480
Ser Ala Leu Ala Ser Ser Ala Ala Thr Ser Asn His His Gln Gly Gly	
145 150 155 160	
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Ser	Ser	Ser	Gly	Arg	Pro	Leu	Asn	Trp	Gly	Ile	Gly	Gly	Gly	Glu	Gly		
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gtt	tct	agg	tca	agt	tta	cca	act	ggg	tta	tgg	cca	aat	gta	gct	ggg	624	
Val	Ser	Arg	Ser	Ser	Leu	Pro	Thr	Gly	Leu	Trp	Pro	Asn	Val	Ala	Gly		
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Phe	Gly	Ser	Gly	Val	Pro	Thr	Thr	Gly	Leu	Met	Ser	Glu	Gly	Ala	Gly		
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Tyr	Arg	Ile	Gly	Phe	Pro	Gly	Phe	Asp	Phe	Pro	Gly	Val	Gly	His	Met		
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Ser	Phe	Ala	Ser	Ile	Leu	Gly	Gly	Asn	His	Asn	Gln	Met	Pro	Gly	Leu		
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Glu	Leu	Gly	Leu	Ser	Gln	Glu	Gly	Asn	Val	Gly	Val	Leu	Asn	Pro	Gln		
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Ser	Phe	Thr	Gln	Ile	Tyr	Gln	Gln	Met	Gly	Gln	Ala	Gln	Ala	Gln	Ala		
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Gln	Gly	Arg	Val	Leu	His	His	Met	His	His	Asn	His	Glu	Glu	His	Gln		
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caa	gag	agt	ggg	gag	aaa	gat	gat	tct	caa	ggc	tca	ggg	cgt			954	
Gln	Glu	Ser	Gly	Glu	Lys	Asp	Asp	Ser	Gln	Gly	Ser	Gly	Arg				
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Thr	Glu	Ile	Lys	Asp	Phe	Gln	Ile	Val	Val	Ser	Ala	Ser	Asp	Lys	Glu
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Arg	Met	Pro	Ala	Leu	Cys	Ala	Ala	Arg	Ile	Phe	Gln	Leu	Thr	Arg	Glu
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Ser	Ser	Ser	Gly	Arg	Pro	Leu	Asn	Trp	Gly	Ile	Gly	Gly	Gly	Glu	Gly
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Phe	Gly	Ser	Gly	Val	Pro	Thr	Thr	Gly	Leu	Met	Ser	Glu	Gly	Ala	Gly
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Glu Leu Gly Leu Ser Gln Glu Gly Asn Val Gly Val Leu Asn Pro Gln  
260 265 270

Ser Phe Thr Gln Ile Tyr Gln Gln Met Gly Gln Ala Gln Ala Gln Ala  
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Glu Asn Arg Gly Asp Asn Val Ala Asn Gly Leu Asn Arg Gln Ile Val  
20 25 30

aga tat cag ccg tcg ata aac gaa gca gca caa aat atg ctt cga cag 144  
Arg Tyr Gln Pro Ser Ile Asn Glu Ala Ala Gln Asn Met Leu Arg Gln  
35 40 45

ttc tta aat act agt acc tca cct cgg tat gaa tca gtt tca aac aat 192  
Phe Leu Asn Thr Ser Thr Ser Pro Arg Tyr Glu Ser Val Ser Asn Asn  
50 55 60

cct gac agt ttc cta ttg ggt gat gtt ccc agt tct acc tct gta gac 240  
Pro Asp Ser Phe Leu Leu Gly Asp Val Pro Ser Ser Thr Ser Val Asp  
65 70 75 80



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Asn Gly Asn Pro Ser Ser Arg Val Ser Gly Val Thr Leu Ala Glu Phe	
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Ser Pro Asn Thr Val Gln Ser Ala Thr Asn Gln Val Pro Glu Ala Ser	
100 105 110	
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Leu Ala His His Pro Gln Ala Gly Leu Val Gln Pro Asn Ile Gly Gln	
115 120 125	
agt ccg gct caa gga gca gca cct gca gac tct tgg agc cct gaa ttt	432
Ser Pro Ala Gln Gly Ala Ala Pro Ala Asp Ser Trp Ser Pro Glu Phe	
130 135 140	
gat tta gtt gga tgc gag aca gat agt gga gag tgt ttt gat cca ata	480
Asp Leu Val Gly Cys Glu Thr Asp Ser Gly Glu Cys Phe Asp Pro Ile	
145 150 155 160	
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Met Ala Val Leu Asp Glu Ser Glu Gly Asp Ala Ile Ser Pro Glu Gly	
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Glu Gly Lys Met Asn Glu Leu Leu Glu Gly Val Pro Lys Leu Pro Gly	
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Ile Gln Asp Pro Phe Trp Glu Gln Phe Phe Ser Val Glu Leu Pro Ala	
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Ile Ala Asp Thr Asp Asp Ile Leu Ser Gly Ser Val Glu Asn Asn Asp	
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Leu Val Leu Glu Gln Glu Pro Asn Glu Trp Thr Arg Asn Glu Gln Gln	
225 230 235 240	
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Phe Leu Asn Thr Ser Thr Ser Pro Arg Tyr Glu Ser Val Ser Asn Asn  
50 55 60

Pro Asp Ser Phe Leu Leu Gly Asp Val Pro Ser Ser Thr Ser Val Asp  
65 70 75 80

Asn Gly Asn Pro Ser Ser Arg Val Ser Gly Val Thr Leu Ala Glu Phe  
85 90 95

Ser Pro Asn Thr Val Gln Ser Ala Thr Asn Gln Val Pro Glu Ala Ser  
100 105 110

Leu Ala His His Pro Gln Ala Gly Leu Val Gln Pro Asn Ile Gly Gln  
115 120 125

Ser Pro Ala Gln Gly Ala Ala Pro Ala Asp Ser Trp Ser Pro Glu Phe  
130 135 140

Asp Leu Val Gly Cys Glu Thr Asp Ser Gly Glu Cys Phe Asp Pro Ile  
145 150 155 160

Met Ala Val Leu Asp Glu Ser Glu Gly Asp Ala Ile Ser Pro Glu Gly  
165 170 175

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Ile Gln Asp Pro Phe Trp Glu Gln Phe Phe Ser Val Glu Leu Pro Ala  
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210 215 220

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<223> Description of Artificial Sequence: primer

<400> 15

cggatccgaa ttcattggaga acgag 25

<210> 16

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 16

cggatccgaa ttctcagaac tgaga 25

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 17

agggatgttt aataccacta c 21

<210> 18

<211> 21  
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 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 18  
 gcacagttga agtgaacttg c 21  
  
  
 <210> 19  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 19  
 cgagatctga attcatggat cagta 25  
  
  
 <210> 20  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 20  
 cgagatctga attcctaagg catgcc 26  
  
  
 <210> 21  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 <400> 21  
 ccatatggaa ttgcgacgag gc 22  
  
  
 <210> 22

<211> 24  
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 <213> Artificial Sequence  
  
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 <400> 22  
 gcagtaatag gatccactat aggg 24  
  
 <210> 23  
 <211> 28  
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 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 23  
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 <210> 24  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 ggggatccaa gacaagataa gagtccctgc cg 32  
  
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 <213> Artificial Sequence  
  
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 <210> 26

<211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 <400> 26  
 ggggatccgc ataaatataa tcaagcagca gcg 33  
  
 <210> 27  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 27  
 gggaattcat gttaaccgca gccggagacg 30  
  
 <210> 28  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 28  
 ggggatccgg ggatccatca aacatataaa gatg 34  
  
 <210> 29  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 29  
 ccgaattcat ggattcccta gcgatttctc c 31  
  
 <210> 30

<211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
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 ggggatccct acaacatgat tcgagaaaat tgatgg 36  
  
 <210> 31  
 <211> 26  
 <212> DNA  
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 <220>  
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 <400> 31  
 gggaattcat ggactctctc gcaacc 26  
  
 <210> 32  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
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 <400> 32  
 ggggatcctt gccgatcagc gtgc 24  
  
 <210> 33  
 <211> 609  
 <212> DNA  
 <213> Arabidopsis thaliana  
  
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 <221> CDS  
 <222> (1)..(606)  
  
 <400> 33  
 atg gcg gaa ctt gag aat cca agt gta atg tcg aag ctg ata gca ttc 48  
 Met Ala Glu Leu Glu Asn Pro Ser Val Met Ser Lys Leu Ile Ala Phe  
 1 5 10 15

tta tct tca ttg cta gag cga gtt gct gag tca aac gat ctg acc cga	96
Leu Ser Ser Leu Leu Glu Arg Val Ala Glu Ser Asn Asp Leu Thr Arg	
20 25 30	
cga gtc gcg act cag tca cag aga gtt tcg gtg ttt cat gga ctg agt	144
Arg Val Ala Thr Gln Ser Gln Arg Val Ser Val Phe His Gly Leu Ser	
35 40 45	
cga cca acg ata acg att cag agc tat cta gag agg atc ttc aaa tac	192
Arg Pro Thr Ile Thr Ile Gln Ser Tyr Leu Glu Arg Ile Phe Lys Tyr	
50 55 60	
gca aat tgt agt cct tct tgc ttc gtc gtt gct tac gtt tat ctc gat	240
Ala Asn Cys Ser Pro Ser Cys Phe Val Val Ala Tyr Val Tyr Leu Asp	
65 70 75 80	
cgt ttc act cac aga caa cct tca ctt ccc atc aat tcc ttt aac gtc	288
Arg Phe Thr His Arg Gln Pro Ser Leu Pro Ile Asn Ser Phe Asn Val	
85 90 95	
cat cgt ctt ctc atc act agt gtc atg gtc gct gct aaa ttc ctc gat	336
His Arg Leu Leu Ile Thr Ser Val Met Val Ala Ala Lys Phe Leu Asp	
100 105 110	
gat ctg tac tac aac aat gcg tat tac gcg aaa gtg gga gga ata agc	384
Asp Leu Tyr Tyr Asn Asn Ala Tyr Tyr Ala Lys Val Gly Gly Ile Ser	
115 120 125	
acg aag gag atg aat ttt cta gag ctg gat ttc tta ttc ggg tta gga	432
Thr Lys Glu Met Asn Phe Leu Glu Leu Asp Phe Leu Phe Gly Leu Gly	
130 135 140	
ttt gaa tta aac gtg acg cca aac aca ttc aac gcc tac ttc tct tat	480
Phe Glu Leu Asn Val Thr Pro Asn Thr Phe Asn Ala Tyr Phe Ser Tyr	
145 150 155 160	
ctt caa aag gaa atg act ctt ctt caa cct ctc tct ctc gtt gtt gtc	528
Leu Gln Lys Glu Met Thr Leu Leu Gln Pro Leu Ser Leu Val Val Val	
165 170 175	
cca tca tca aga tct ctc att acc ttc aac gac gat gaa gct tct cat	576
Pro Ser Ser Arg Ser Leu Ile Thr Phe Asn Asp Asp Glu Ala Ser His	
180 185 190	
cag aaa caa caa caa caa caa ctc gct gtt tga	609
Gln Lys Gln Gln Gln Gln Gln Leu Ala Val	
195 200	



<210> 34

<211> 202

<212> PRT

<213> Arabidopsis thaliana

<400> 34

Met Ala Glu Leu Glu Asn Pro Ser Val Met Ser Lys Leu Ile Ala Phe  
1 5 10 15

Leu Ser Ser Leu Leu Glu Arg Val Ala Glu Ser Asn Asp Leu Thr Arg  
20 25 30

Arg Val Ala Thr Gln Ser Gln Arg Val Ser Val Phe His Gly Leu Ser  
35 40 45

Arg Pro Thr Ile Thr Ile Gln Ser Tyr Leu Glu Arg Ile Phe Lys Tyr  
50 55 60

Ala Asn Cys Ser Pro Ser Cys Phe Val Val Ala Tyr Val Tyr Leu Asp  
65 70 75 80

Arg Phe Thr His Arg Gln Pro Ser Leu Pro Ile Asn Ser Phe Asn Val  
85 90 95

His Arg Leu Leu Ile Thr Ser Val Met Val Ala Ala Lys Phe Leu Asp  
100 105 110

Asp Leu Tyr Tyr Asn Asn Ala Tyr Tyr Ala Lys Val Gly Gly Ile Ser  
115 120 125

Thr Lys Glu Met Asn Phe Leu Glu Leu Asp Phe Leu Phe Gly Leu Gly  
130 135 140

Phe Glu Leu Asn Val Thr Pro Asn Thr Phe Asn Ala Tyr Phe Ser Tyr  
145 150 155 160

Leu Gln Lys Glu Met Thr Leu Leu Gln Pro Leu Ser Leu Val Val Val  
165 170 175

Pro Ser Ser Arg Ser Leu Ile Thr Phe Asn Asp Asp Glu Ala Ser His  
180 185 190

Gln Lys Gln Gln Gln Gln Leu Ala Val  
195 200

<210> 35  
 <211> 660  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(657)

<400> 35

atg gct gat cag att gag atc cag aga atg aac caa gat ctt caa gaa	48
Met Ala Asp Gln Ile Glu Ile Gln Arg Met Asn Gln Asp Leu Gln Glu	
1 5 10 15	
cca ttg gct gag atc atg cca agt gtt tta acg gca atg tcg tat ctc	96
Pro Leu Ala Glu Ile Met Pro Ser Val Leu Thr Ala Met Ser Tyr Leu	
20 25 30	
ttg caa aga gta tcg gag acc aac gac aac ctg agc cag aaa cag aag	144
Leu Gln Arg Val Ser Glu Thr Asn Asp Asn Leu Ser Gln Lys Gln Lys	
35 40 45	
ccc tca agc ttc act gga gta acc aaa cct tcc att tcc atc aga agc	192
Pro Ser Ser Phe Thr Gly Val Thr Lys Pro Ser Ile Ser Ile Arg Ser	
50 55 60	
tat ctc gaa cgg atc ttt gaa tac gcg aat tgt agc tac tcg tgt tac	240
Tyr Leu Glu Arg Ile Phe Glu Tyr Ala Asn Cys Ser Tyr Ser Cys Tyr	
65 70 75 80	
atc gtc gca tat ata tat ttg gat cgg ttc gtg aag aag cag cca ttt	288
Ile Val Ala Tyr Ile Tyr Leu Asp Arg Phe Val Lys Lys Gln Pro Phe	
85 90 95	
ttg cct atc aat tct ttt aat gtc cat agg ctt ata atc aca agt gtc	336
Leu Pro Ile Asn Ser Phe Asn Val His Arg Leu Ile Ile Thr Ser Val	
100 105 110	
ttg gtc tct gct aaa ttc atg gat gac ttg agt tac aac aat gaa tat	384
Leu Val Ser Ala Lys Phe Met Asp Asp Leu Ser Tyr Asn Asn Glu Tyr	
115 120 125	
tat gca aaa gtt gga gga ata agc aga gaa gaa atg aac atg ctt gag	432
Tyr Ala Lys Val Gly Gly Ile Ser Arg Glu Glu Met Asn Met Leu Glu	
130 135 140	
ctt gac ttc ttg ttc gga att ggg ttt gag tta aac gtc acc gtt tct	480

Leu Asp Phe Leu Phe Gly Ile Gly Phe Glu Leu Asn Val Thr Val Ser  
 145 150 155 160  
  
 act ttc aat aac tat tgt tgt ttt cta caa aga gag atg gcg atg ttg 528  
 Thr Phe Asn Asn Tyr Cys Cys Phe Leu Gln Arg Glu Met Ala Met Leu  
 165 170 175  
  
 atg aag atg aag tct ctg ttt ctt gaa cct tct tca ttc aaa atc tct 576  
 Met Lys Met Lys Ser Leu Phe Leu Glu Pro Ser Ser Phe Lys Ile Ser  
 180 185 190  
  
 ttt aag acg aaa ctt gtg atg tat cca cac gag gaa gac tct tta tct 624  
 Phe Lys Thr Lys Leu Val Met Tyr Pro His Glu Glu Asp Ser Leu Ser  
 195 200 205  
  
 act cac cac aac aag aag caa ctc gct gct gct tga 660  
 Thr His His Asn Lys Lys Gln Leu Ala Ala Ala  
 210 215  
  
 <210> 36  
 <211> 219  
 <212> PRT  
 <213> Arabidopsis thaliana  
  
 <400> 36  
 Met Ala Asp Gln Ile Glu Ile Gln Arg Met Asn Gln Asp Leu Gln Glu  
 1 5 10 15  
  
 Pro Leu Ala Glu Ile Met Pro Ser Val Leu Thr Ala Met Ser Tyr Leu  
 20 25 30  
  
 Leu Gln Arg Val Ser Glu Thr Asn Asp Asn Leu Ser Gln Lys Gln Lys  
 35 40 45  
  
 Pro Ser Ser Phe Thr Gly Val Thr Lys Pro Ser Ile Ser Ile Arg Ser  
 50 55 60  
  
 Tyr Leu Glu Arg Ile Phe Glu Tyr Ala Asn Cys Ser Tyr Ser Cys Tyr  
 65 70 75 80  
  
 Ile Val Ala Tyr Ile Tyr Leu Asp Arg Phe Val Lys Lys Gln Pro Phe  
 85 90 95  
  
 Leu Pro Ile Asn Ser Phe Asn Val His Arg Leu Ile Ile Thr Ser Val  
 100 105 110  
  
 Leu Val Ser Ala Lys Phe Met Asp Asp Leu Ser Tyr Asn Asn Glu Tyr

115		120		125
Tyr Ala Lys Val Gly Gly Ile Ser Arg Glu Glu Met Asn Met Leu Glu				
130		135		140
Leu Asp Phe Leu Phe Gly Ile Gly Phe Glu Leu Asn Val Thr Val Ser				
145		150		155 160
Thr Phe Asn Asn Tyr Cys Cys Phe Leu Gln Arg Glu Met Ala Met Leu				
	165		170	175
Met Lys Met Lys Ser Leu Phe Leu Glu Pro Ser Ser Phe Lys Ile Ser				
	180		185	190
Phe Lys Thr Lys Leu Val Met Tyr Pro His Glu Glu Asp Ser Leu Ser				
	195		200	205
Thr His His Asn Lys Lys Gln Leu Ala Ala Ala				
210		215		

<210> 37  
 <211> 633  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(630)

<400> 37	
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Met Leu Thr Ala Ala Gly Asp Asp Glu Leu Asp Pro Val Val Gly Pro	
1 5 10 15	
gaa tcg gca acg gaa gca gcc act cca aga gtg ctg act ata atc tcc	96
Glu Ser Ala Thr Glu Ala Ala Thr Pro Arg Val Leu Thr Ile Ile Ser	
20 25 30	
cat gtg atg gag aag ctc gtg gca cga aac gag tgg tta gct aag caa	144
His Val Met Glu Lys Leu Val Ala Arg Asn Glu Trp Leu Ala Lys Gln	
35 40 45	
act aag gga ttt ggg aag agc ttg gag gcg ttt cac ggc gtg aga gcg	192
Thr Lys Gly Phe Gly Lys Ser Leu Glu Ala Phe His Gly Val Arg Ala	
50 55 60	

ccg agc ata agt ata gct aaa tac ctt gag agg ata tat aag tac aca 240  
 Pro Ser Ile Ser Ile Ala Lys Tyr Leu Glu Arg Ile Tyr Lys Tyr Thr  
 65 70 75 80

aaa tgt agc ccg gca tgt ttc gtt gtt ggg tat gtg tac ata gac cgg 288  
 Lys Cys Ser Pro Ala Cys Phe Val Val Gly Tyr Val Tyr Ile Asp Arg  
 85 90 95

ttg gct cat aag cat cct ggt tct ttg gtt gtc tcc ttg aat gtt cat 336  
 Leu Ala His Lys His Pro Gly Ser Leu Val Val Ser Leu Asn Val His  
 100 105 110

aga ctc ctc gtc act tgt gtc atg att gct gcc aag ata cta gat gac 384  
 Arg Leu Leu Val Thr Cys Val Met Ile Ala Ala Lys Ile Leu Asp Asp  
 115 120 125

gtg cac tac aac aac gag ttc tat gct cgg gtt gga ggc gta agc aat 432  
 Val His Tyr Asn Asn Glu Phe Tyr Ala Arg Val Gly Gly Val Ser Asn  
 130 135 140

gca gac ttg aac aaa atg gag ttg gag ctt ctc ttt ctt ctt gac ttt 480  
 Ala Asp Leu Asn Lys Met Glu Leu Glu Leu Leu Phe Leu Leu Asp Phe  
 145 150 155 160

aga gtt act gtg agt ttt aga gtt ttc gag agc tat tgc ttt cac ctc 528  
 Arg Val Thr Val Ser Phe Arg Val Phe Glu Ser Tyr Cys Phe His Leu  
 165 170 175

gaa aaa gag atg caa cta aac gac gtc gtt tct tcc ctc aaa gat att 576  
 Glu Lys Glu Met Gln Leu Asn Asp Val Val Ser Ser Leu Lys Asp Ile  
 180 185 190

caa cca atg caa gaa agt ctc tct cca gca tct act tta tca tct tta 624  
 Gln Pro Met Gln Glu Ser Leu Ser Pro Ala Ser Thr Leu Ser Ser Leu  
 195 200 205

tat gtt tga 633  
 Tyr Val  
 210

<210> 38

<211> 210

<212> PRT

<213> Arabidopsis thaliana

<400> 38

Met Leu Thr Ala Ala Gly Asp Asp Glu Leu Asp Pro Val Val Gly Pro

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Glu Ser Ala Thr Glu Ala Ala Thr Pro Arg Val Leu Thr Ile Ile Ser			
20	25	30	
His Val Met Glu Lys Leu Val Ala Arg Asn Glu Trp Leu Ala Lys Gln			
35	40	45	
Thr Lys Gly Phe Gly Lys Ser Leu Glu Ala Phe His Gly Val Arg Ala			
50	55	60	
Pro Ser Ile Ser Ile Ala Lys Tyr Leu Glu Arg Ile Tyr Lys Tyr Thr			
65	70	75	80
Lys Cys Ser Pro Ala Cys Phe Val Val Gly Tyr Val Tyr Ile Asp Arg			
85	90	95	
Leu Ala His Lys His Pro Gly Ser Leu Val Val Ser Leu Asn Val His			
100	105	110	
Arg Leu Leu Val Thr Cys Val Met Ile Ala Ala Lys Ile Leu Asp Asp			
115	120	125	
Val His Tyr Asn Asn Glu Phe Tyr Ala Arg Val Gly Gly Val Ser Asn			
130	135	140	
Ala Asp Leu Asn Lys Met Glu Leu Glu Leu Leu Phe Leu Leu Asp Phe			
145	150	155	160
Arg Val Thr Val Ser Phe Arg Val Phe Glu Ser Tyr Cys Phe His Leu			
165	170	175	
Glu Lys Glu Met Gln Leu Asn Asp Val Val Ser Ser Leu Lys Asp Ile			
180	185	190	
Gln Pro Met Gln Glu Ser Leu Ser Pro Ala Ser Thr Leu Ser Ser Leu			
195	200	205	
Tyr Val			
210			

<210> 39

<211> 669

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(666)

<400> 39

atg gat tcc cta gcg att tct cca agg aag ctc cga tca gac ctc tac	48
Met Asp Ser Leu Ala Ile Ser Pro Arg Lys Leu Arg Ser Asp Leu Tyr	
1 5 10 15	
tct tac tct tac caa gat gat tcc aac aca gta cct cta gtc atc tct	96
Ser Tyr Ser Tyr Gln Asp Asp Ser Asn Thr Val Pro Leu Val Ile Ser	
20 25 30	
gtt ctc tcg tct ctg atc gaa cga act tta gct agg aac gag aga atc	144
Val Leu Ser Ser Leu Ile Glu Arg Thr Leu Ala Arg Asn Glu Arg Ile	
35 40 45	
agc cgg agc tac ggt ggt ttt ggt aag aca cgt gtc ttt gat tgc cgg	192
Ser Arg Ser Tyr Gly Gly Phe Gly Lys Thr Arg Val Phe Asp Cys Arg	
50 55 60	
gag att cct gat atg act att caa tca tac cta gag aga att ttc cgg	240
Glu Ile Pro Asp Met Thr Ile Gln Ser Tyr Leu Glu Arg Ile Phe Arg	
65 70 75 80	
tat acc aaa gcc ggt cca tcg gtt tac gtc gtg gct tat gta tac att	288
Tyr Thr Lys Ala Gly Pro Ser Val Tyr Val Val Ala Tyr Val Tyr Ile	
85 90 95	
gac cgg ttc tgt cag aat aac caa ggt ttc aga atc agt ctt acc aat	336
Asp Arg Phe Cys Gln Asn Asn Gln Gly Phe Arg Ile Ser Leu Thr Asn	
100 105 110	
gta cat cgt ctc ctt atc aca act atc atg atc gct tcc aaa tac gtc	384
Val His Arg Leu Leu Ile Thr Thr Ile Met Ile Ala Ser Lys Tyr Val	
115 120 125	
gaa gat atg aac tac aaa aac tcg tac ttt gcg aaa gta gga gga tta	432
Glu Asp Met Asn Tyr Lys Asn Ser Tyr Phe Ala Lys Val Gly Gly Leu	
130 135 140	
gag aca gaa gat ttg aac aat ttg gaa ctg gag ttc ttg ttc ttg atg	480
Glu Thr Glu Asp Leu Asn Asn Leu Glu Leu Glu Phe Leu Phe Leu Met	
145 150 155 160	
gga ttt aag ttg cat gtg aat gtg agt gtg ttc gag agt tac tgt tgt	528
Gly Phe Lys Leu His Val Asn Val Ser Val Phe Glu Ser Tyr Cys Cys	
165 170 175	

cat cta gaa aga gaa gtg agt att gga gga ggt tat cag atc gaa aaa 576  
 His Leu Glu Arg Glu Val Ser Ile Gly Gly Gly Tyr Gln Ile Glu Lys  
                   180                  185                  190

gca ttg cgt tgc gct gag gaa atc aaa tct aga caa att gtt caa gac 624  
 Ala Leu Arg Cys Ala Glu Glu Ile Lys Ser Arg Gln Ile Val Gln Asp  
                   195                  200                  205

cct aaa cat cat cat cac cat caa ttt tct cga atc atg ttg tag 669  
 Pro Lys His His His His His Gln Phe Ser Arg Ile Met Leu  
                   210                  215                  220

<210> 40

<211> 222

<212> PRT

<213> Arabidopsis thaliana

<400> 40

Met Asp Ser Leu Ala Ile Ser Pro Arg Lys Leu Arg Ser Asp Leu Tyr  
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Ser Tyr Ser Tyr Gln Asp Asp Ser Asn Thr Val Pro Leu Val Ile Ser  
                   20                  25                  30

Val Leu Ser Ser Leu Ile Glu Arg Thr Leu Ala Arg Asn Glu Arg Ile  
                   35                  40                  45

Ser Arg Ser Tyr Gly Gly Phe Gly Lys Thr Arg Val Phe Asp Cys Arg  
                   50                  55                  60

Glu Ile Pro Asp Met Thr Ile Gln Ser Tyr Leu Glu Arg Ile Phe Arg  
                   65                  70                  75                  80

Tyr Thr Lys Ala Gly Pro Ser Val Tyr Val Val Ala Tyr Val Tyr Ile  
                   85                  90                  95

Asp Arg Phe Cys Gln Asn Asn Gln Gly Phe Arg Ile Ser Leu Thr Asn  
                   100                  105                  110

Val His Arg Leu Leu Ile Thr Thr Ile Met Ile Ala Ser Lys Tyr Val  
                   115                  120                  125

Glu Asp Met Asn Tyr Lys Asn Ser Tyr Phe Ala Lys Val Gly Gly Leu  
                   130                  135                  140

Glu Thr Glu Asp Leu Asn Asn Leu Glu Leu Glu Phe Leu Phe Leu Met



145                      150                      155                      160  
 Gly Phe Lys Leu His Val Asn Val Ser Val Phe Glu Ser Tyr Cys Cys  
                          165                      170                      175  
 His Leu Glu Arg Glu Val Ser Ile Gly Gly Gly Tyr Gln Ile Glu Lys  
                          180                      185                      190  
 Ala Leu Arg Cys Ala Glu Glu Ile Lys Ser Arg Gln Ile Val Gln Asp  
                          195                      200                      205  
 Pro Lys His His His His His Gln Phe Ser Arg Ile Met Leu  
                          210                      215                      220

<210> 41  
 <211> 671  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(663)

<400> 41  
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 Met Asp Ser Leu Ala Thr Asp Pro Ala Phe Ile Asp Ser Asp Val Tyr  
   1                          5                          10                          15  
  
 ctc agg tta gga ctt att att gag ggc aaa cga ttg aaa aag cca ccg    96  
 Leu Arg Leu Gly Leu Ile Ile Glu Gly Lys Arg Leu Lys Lys Pro Pro  
                           20                          25                          30  
  
 act gta ctc tca cgc ctc tct tct tct ctg gag aga tct ctg tta ctc    144  
 Thr Val Leu Ser Arg Leu Ser Ser Ser Leu Glu Arg Ser Leu Leu Leu  
                           35                          40                          45  
  
 aat cat gat gac aag att ctg ctt gga tcg cca gac tct gtt acc gtg    192  
 Asn His Asp Asp Lys Ile Leu Leu Gly Ser Pro Asp Ser Val Thr Val  
                           50                          55                          60  
  
 ttt gac ggg aga tct ccc cct gag atc agt att gca cac tac ttg gat    240  
 Phe Asp Gly Arg Ser Pro Pro Glu Ile Ser Ile Ala His Tyr Leu Asp  
   65                          70                          75                          80  
  
 cgc att ttc aag tac tct tgc tgc agt ccc tcc tgc ttc gtc att gcg    288  
 Arg Ile Phe Lys Tyr Ser Cys Cys Ser Pro Ser Cys Phe Val Ile Ala

85

90

95

cat atc tac att gat cac ttt ctc cat aag acc cga gcc ctt ctc aaa 336  
 His Ile Tyr Ile Asp His Phe Leu His Lys Thr Arg Ala Leu Leu Lys  
                   100                                  105                                  110

ccc ctt aat gtc cac cgc ctt atc att aca act gtc atg tta gct gct 384  
 Pro Leu Asn Val His Arg Leu Ile Ile Thr Thr Val Met Leu Ala Ala  
                   115                                  120                                  125

aaa gtc ttc gat gat agg tat ttc aac aat gca tac tac gca aga gtg 432  
 Lys Val Phe Asp Asp Arg Tyr Phe Asn Asn Ala Tyr Tyr Ala Arg Val  
                   130                                  135                                  140

gga ggt gtg act acg aga gag tta aac aga ttg gag atg gag ttg ttg 480  
 Gly Gly Val Thr Thr Arg Glu Leu Asn Arg Leu Glu Met Glu Leu Leu  
                   145                                  150                                  155                                  160

ttt acc ctt gac ttc aag ctt cag gta gat cct cag acg ttt cac aca 528  
 Phe Thr Leu Asp Phe Lys Leu Gln Val Asp Pro Gln Thr Phe His Thr  
                                   165                                  170                                  175

cac tgt tgt cag tta gaa aag cag aac aga gac ggc ttc cag atc gag 576  
 His Cys Cys Gln Leu Glu Lys Gln Asn Arg Asp Gly Phe Gln Ile Glu  
                                   180                                  185                                  190

tgg ccc ata aaa gaa gca tgc cga gcc aac aaa gag act tgg cag aag 624  
 Trp Pro Ile Lys Glu Ala Cys Arg Ala Asn Lys Glu Thr Trp Gln Lys  
                   195                                  200                                  205

agg aca ccc gac tca ctc tgc tct caa acc aca gca cgc tgatcggc 671  
 Arg Thr Pro Asp Ser Leu Cys Ser Gln Thr Thr Ala Arg  
                   210                                  215                                  220

<210> 42

<211> 221

<212> PRT

<213> Arabidopsis thaliana

<400> 42

Met Asp Ser Leu Ala Thr Asp Pro Ala Phe Ile Asp Ser Asp Val Tyr  
           1                                  5                                  10                                  15

Leu Arg Leu Gly Leu Ile Ile Glu Gly Lys Arg Leu Lys Lys Pro Pro  
                   20                                  25                                  30

Thr Val Leu Ser Arg Leu Ser Ser Ser Leu Glu Arg Ser Leu Leu Leu

35	40	45
Asn His Asp Asp Lys Ile Leu Leu Gly Ser Pro Asp Ser Val Thr Val		
50	55	60
Phe Asp Gly Arg Ser Pro Pro Glu Ile Ser Ile Ala His Tyr Leu Asp		
65	70	75 80
Arg Ile Phe Lys Tyr Ser Cys Cys Ser Pro Ser Cys Phe Val Ile Ala		
	85 90	95
His Ile Tyr Ile Asp His Phe Leu His Lys Thr Arg Ala Leu Leu Lys		
100	105	110
Pro Leu Asn Val His Arg Leu Ile Ile Thr Thr Val Met Leu Ala Ala		
115	120	125
Lys Val Phe Asp Asp Arg Tyr Phe Asn Asn Ala Tyr Tyr Ala Arg Val		
130	135	140
Gly Gly Val Thr Thr Arg Glu Leu Asn Arg Leu Glu Met Glu Leu Leu		
145	150	155 160
Phe Thr Leu Asp Phe Lys Leu Gln Val Asp Pro Gln Thr Phe His Thr		
	165 170	175
His Cys Cys Gln Leu Glu Lys Gln Asn Arg Asp Gly Phe Gln Ile Glu		
180	185	190
Trp Pro Ile Lys Glu Ala Cys Arg Ala Asn Lys Glu Thr Trp Gln Lys		
195	200	205
Arg Thr Pro Asp Ser Leu Cys Ser Gln Thr Thr Ala Arg		
210	215	220

<210> 43

<211> 85

<212> PRT

<213> Arabidopsis thaliana

<400> 43

Tyr Leu Glu Arg Ile Phe Lys Tyr Ala Asn Cys Ser Pro Ser Cys Phe
1 5 10 15

Val Val Ala Tyr Val Tyr Leu Asp Arg Phe Thr His Arg Gln Pro Ser
20 25 30

Leu Pro Ile Asn Ser Phe Asn Val His Arg Leu Leu Ile Thr Ser Val  
 35 40 45

Met Val Ala Ala Lys Phe Leu Asp Asp Leu Tyr Tyr Asn Asn Ala Tyr  
 50 55 60

Tyr Ala Lys Val Gly Gly Ile Ser Thr Lys Glu Met Asn Phe Leu Glu  
 65 70 75 80

Leu Asp Phe Leu Phe  
 85

<210> 44

<211> 85

<212> PRT

<213> Arabidopsis thaliana

<400> 44

Tyr Leu Glu Arg Ile Phe Glu Tyr Ala Asn Cys Ser Tyr Ser Cys Tyr  
 1 5 10 15

Ile Val Ala Tyr Ile Tyr Leu Asp Arg Phe Val Lys Lys Gln Pro Phe  
 20 25 30

Leu Pro Ile Asn Ser Phe Asn Val His Arg Leu Ile Ile Thr Ser Val  
 35 40 45

Leu Val Ser Ala Lys Phe Met Asp Asp Leu Ser Tyr Asn Asn Glu Tyr  
 50 55 60

Tyr Ala Lys Val Gly Gly Ile Ser Arg Glu Glu Met Asn Met Leu Glu  
 65 70 75 80

Leu Asp Phe Leu Phe  
 85

<210> 45

<211> 85

<212> PRT

<213> Arabidopsis thaliana

<400> 45

Tyr Leu Glu Arg Ile Tyr Lys Tyr Thr Lys Cys Ser Pro Ala Cys Phe  
 1 5 10 15

Val Val Gly Tyr Val Tyr Ile Asp Arg Leu Ala His Lys His Pro Gly  
20 25 30

Ser Leu Val Val Ser Leu Asn Val His Arg Leu Leu Val Thr Cys Val  
35 40 45

Met Ile Ala Ala Lys Ile Leu Asp Asp Val His Tyr Asn Asn Glu Phe  
50 55 60

Tyr Ala Arg Val Gly Gly Val Ser Asn Ala Asp Leu Asn Lys Met Glu  
65 70 75 80

Leu Glu Leu Leu Phe  
85

<210> 46

<211> 85

<212> PRT

<213> Arabidopsis thaliana

<400> 46

Tyr Leu Glu Arg Ile Phe Arg Tyr Thr Lys Ala Gly Pro Ser Val Tyr  
1 5 10 15

Val Val Ala Tyr Val Tyr Ile Asp Arg Phe Cys Gln Asn Asn Gln Gly  
20 25 30

Phe Arg Ile Ser Leu Thr Asn Val His Arg Leu Leu Ile Thr Thr Ile  
35 40 45

Met Ile Ala Ser Lys Tyr Val Glu Asp Met Asn Tyr Lys Asn Ser Tyr  
50 55 60

Phe Ala Lys Val Gly Gly Leu Glu Thr Glu Asp Leu Asn Asn Leu Glu  
65 70 75 80

Leu Glu Phe Leu Phe  
85

<210> 47

<211> 84

<212> PRT

<213> Arabidopsis thaliana

<400> 47

Tyr Leu Asp Arg Ile Phe Lys Tyr Ser Cys Cys Ser Pro Ser Cys Phe

1                      5                      10                      15  
 Val Ile Ala His Ile Tyr Ile Asp His Phe Leu His Lys Thr Arg Ala  
                     20                      25                      30  
 Leu Leu Lys Pro Leu Asn Val His Arg Leu Ile Ile Thr Thr Val Met  
                     35                      40                      45  
 Leu Ala Ala Lys Val Phe Asp Asp Arg Tyr Phe Asn Asn Ala Tyr Tyr  
                     50                      55                      60  
 Ala Arg Val Gly Gly Val Thr Thr Arg Glu Leu Asn Arg Leu Glu Met  
                     65                      70                      75                      80  
 Glu Leu Leu Phe

<210> 48  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 48  
 attgcacact acttgatcg catt 24

<210> 49  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 49  
 gatagaatgg gaacggctag 20

<210> 50  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 'primer

<400> 50

ctgataccag acgttgcccg cataa

25

<210> 51

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 51

ctacaaattg ccttttctta tcgac

25

<210> 52

<211> 572

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (1)

<223> n at position 1 can be a, t, g, or c.

<220>

<221> unsure

<222> (18)

<223> n at position 18 can be a, t, g, or c.

<220>

<221> unsure

<222> (231)

<223> n at position 231 can be a, t, g, or c.

<220>

<221> unsure

<222> (412)

<223> n at position 412 can be a, t, g, or c.

<220>

<221> unsure

<222> (473)  
<223> n at position 473 can be a, t, g, or c.

<220>  
<221> unsure  
<222> (473)  
<223> n at position 473 can be a, t, g, or c.

<220>  
<221> unsure  
<222> (495)  
<223> n at position 495 can be a, t, g, or c.

<220>  
<221> unsure  
<222> (543)  
<223> n at position 543 can be a, t, g, or c.

<220>  
<221> unsure  
<222> (557)  
<223> n at position 557 can be a, t, g, or c.

<220>  
<221> unsure  
<222> (561)  
<223> n at position 561 can be a, t, g, or c.

<220>  
<221> unsure  
<222> (562)  
<223> n at position 562 can be a, t, g, or c.

<220>  
<221> unsure  
<222> (570)  
<223> n at position 570 can be a, t, g, or c.

<400> 52  
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ccataagacc cgagcccttc tcaaaccctt taatgtccac cgccttatca ttacaactgt 120  
catgttagct gctaaagtct tcgatgatag gtatgttact cactaaacct ggtatcaaat 180  
tcaacacgca aataagtctt caatcataga ttcatgtgat tctgggtgttg ngcaggtatt 240  
tcaacaatgc atactacgca agagtgggag gtgtgactac gagagagtta aacagattgg 300  
agatggagtt gttgtttacc cttgacttca agcttcaggt agatcctcag acgtttcaca 360  
cacactgttg tactgaatcg gattttcaag ggtctggcca aaactattcc gngggcacct 420  
ggcacacgcc ctggagtccg gcccgtttcc agttgagggt tgtctacgct tanatgagaa 480  
ggaaagttgt ccaanacgaa tcccagtgtc ctattaccaa tagccgacgg tatcgataag 540



ctngatgtac atggtcnata nnaaaaggcn at

572

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 53

cgatccagct ttcattgatt cg

22

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 54

gatagaatgg gaacggctag

20

<210> 55

<211> 740

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (6)

<223> n at position 6 can be a, t, g, or c.

<220>

<221> unsure

<222> (9)

<223> n at position 9 can be a, t, g, or c.

<220>

<221> unsure

<222> (11)

<223> n at position 11 can be a, t, g, or c.

<220>

<221> unsure

<222> (733)

<223> n at position 733 can be a, t, g, or c.

<220>

<221> unsure

<222> (738)

<223> n at position 738 can be a, t, g, or c.

<400> 55

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atttcnttng ntgtatacct caggtttagga cttattattg agggcaaacg attgaaaaag 60
ccaccgactg ttctctcacg cctctcttct tctctggaga gatctctggt actcaatcat 120
gatgacaaga ttctgcttgg atcgccagac tctgttaccg tgtttgacgg gagatctccc 180
cctgagatca gtattgcaca ctacttggat cgcattttca agtactcttg ctgcagtccc 240
tctgcttcg tcattgcga tatctacatt gatcactttc tccataagac ccgagccctt 300
ctcaaaccct ttaatgtcca ccgccttata attacaactg tcatgttagc tgctaaagtc 360
ttcgatgata ggtatgttac tcaactaaacc tggatatcaa ttcaacacgc aaataagtct 420
tcaatcatag attcattgat ctctggtggt gtgcaggat ttcaacaatg catactacgc 480
aagagtggga ggtgtgacta cgagagagtt aaacagattg gagatggagt tgttggtttac 540
ccttgacttc aagcttcagg tagatcctca gacgtttcac acacactggt gtcaagttag 600
aaaagcagaa cagcgacggc ttccagatcg agtggcccat aaaagaagca tgccgagcca 660
acaaagagac ttggcagaag aggacacccg actcactctg ctctcaaacc acagcacgct 720
gatcggcaag ggnaaaanga 740
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<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<223> n at positions 6, 9, 11, 733 and 738 can be a, t,  
g or c.

<400> 56

attgcacact acttgatcg catt

24

<210> 57

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 57

ctatcttacc cttgccgac agc

23

<210> 58

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 58

ctacaaattg ccttttctta tcgac

25